

Don't Let Your Kids Grow Up Without You

5 The following sequences are presented:

SEQ ID No. 1 = murine amino acid sequence

SEQ ID No. 2 = murine coding nucleotide sequence

10 SEQ ID No. 3 = truncated human amino acid sequence

SEQ ID No. 4 = truncated human coding nucleotide sequence

SEQ ID No. 5 = human amino acid sequence

SEQ ID No. 6 = human coding nucleotide sequence

15

SEQ ID No. 7 = murine cDNA sequence

SEQ ID No. 8 = truncated human cDNA sequence

20 SEQ ID No. 9 = Formula I

(It is to be noted that in the above text, references to SEQ ID No. 2 are equally applicable to SEQ ID No. 7. Also, references to SEQ ID No. 4 or SEQ ID No. 6 are equally applicable to SEQ ID No. 8.)

PC10315AGPR
SEQ ID No. 1

95

MSCLMVERCGEVLFESEPEQSVKVCMLGDVRLRGQTGVPAERRGSYPFIDFRLNNTTHSGEIGTKKKVK 70
RLLSFQRYFHASRLLRGIIPQAPLHLLDEYLGQARHMLSKVGTWDFDIFLFDRLTNGNSLVTLCHLFN 140
5 SHGLIHFFKLDVMTLHRFLVMVQEDYHGHNPYHNAVHAADVQAMHCYLKEPKLASFLTPLDIMLGLLAA 210
AAHDVDHPGVNQPFILKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLIL 280
ATDINRQNEFLTRLKAHLHNKDLRLENVQDRHFMLQIALKCADICNPCRIMWEMSKQWSEVCEEFYRQGD 350
LEQKFELEISPLCNQKDSIPSIQIGFMTYIVEPLFREWARFTGNSTLSENMLSHLAHNKAQWKSLLSNQ 420
HRRRGSGQDLGAPAPETLEQTEGATP 446

SEQ ID No. 2

start

15 ATGTCTTGTTTAATGGTTGAGAGGTGTGGCGAAGTCTTGTTTGAGAGCCCTGAACAGAGTGTCAAA
TGTGTTTGCATGCTAGGAGATGTACGACTAAGGGGTGACACGGGGTTCCTGCCGAACGCCGTGGCTCCT
ACCCATTTCATTGACTTCCGTCTACTTAACAATACAACACACTCAGGGGAAATTGGCACCAAGAAAAAGGT
GAAACGACTGTTAAGTTTCCAAAGATACTTCCATGCATCTAGGCTTCTCCGGGGGATTATACCGCAGGCC
CCTCTCCACCTGCTGGATGAAGACTACCTTGGACAAGCAAGGCACATGCTCTCCAAAGTTGGAACGTGGG
ACTTTGACATTTTCTTGTGATCGCTTGACAAATGGGAACAGTCTGGTAACCTCTGTTGTGTCACCTCTT
20 CAACTCCCATGGGCTCATCCACCATTTCAGCTCGATATGGTGACCTTGCACAGGTTTCTGGTTATGGTT
CAGGAAGATTACCACGGTCACAACCCATACCACAATGCTGTTCACGCAGCCGACGTACCCAGGCCATGC
ACTGTTACCTGAAGGAGCCAAAGTTGGCAAGCTTCCTCACACCTCTGGACATCATGCTTGGACTACTGGC
TGCAGCAGCTCATGACGTGGACCACCCAGGGGTCAACCAGCCATTTTGTATCAAACTAACCACCATCTT
GCCAACCTGTATCAGAATATGTCTGTACTGGAGAATCACCCTGGCGATCTACAATTGGCATGCTTCGAG
25 AATCACGGCTCCTGGCTCACTTGCCAAAGGAAATGACACAGGATATCGAACAGCAGCTGGGCTCCCTCAT
CTTGGCCACGGATATCAACAGACAGAATGAGTTTCTGACCCGCTTAAAAGCTCACCTCCACAATAAAGAT
TTGAGACTGGAGAATGTACAGGACAGACACTTTATGCTTCAGATCGCCTTGAAGTGTGCTGACATTTGCA
ATCCTTGTCTGATCTGGGAGATGAGCAAGCAGTGGAGTGAAAGGGTCTGTGAGGAATTCTACAGACAAGG
TGACCTTGAACAGAAGTTTGAAGTGGAAATCAGTCCCTCTTTGTAATCAACAGAAAGATTCAATCCCTAGC
30 ATACAAATTGGTTTTCATGACTTACATCGTGGAGCCGCTGTTCCGGGAGTGGGCCCCGTTTACTGGGAACA
GCACCTGTGCGGAGAACATGCTAAGCCATCTCGCGCACAAAGGCCAGTGGAAGAGCCTGCTGTCCAA
TCAGCACAGACGCGAGGGCAGCGCCAGGACCTGGCGGGCCCCGCACCTGAGACCCTGGAGCAGACAGAA
GGTGCCACGCCCTAA

stop

SEQ ID No. 3

40 MSCLMVERCGEILFENPDQNAKVCMLGDIRLRGQTGVRAERRGSYPFIDFRLNSTTYSGEIGTKKKVK 70
RLLSFQRYFHASRLLRGIIPQAPLHLLDEYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLCHLFN 140
THGLIHFFKLDVMTLHRFLVMVQEDYHSQNPYHNAVHAADVQAMHCYLKEPKLASFLTPLDIMLGLLAA 210
AAHDVDHPGVNQPFILKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMTGTWDFDIFLFDRL 280
LTNGNSLV 288

SEQ ID No. 4

start

50 ATGTCTTGTTTAATGGTTGAGAGGTGTGGCGAAATCTTGTTTGAGAACCCCGA
TCAGAATGCCAAATGTGTTTGCATGCTGGGAGATATACGACTAAGGGGTGACACGGGGTTCGTGCTGAA
CGCCGTGGCTCCTACCCATTTCATTGACTTCCGCCTACTTAACAGTACAACATACTCAGGGGAGATTGGCA
CCAAGAAAAAGGTGAAAAGACTATTAAGCTTTCAAAGATACTTCCATGCATCAAGGCTGCTTCGTGGAAT
TATACCACAAGCCCCCTGACCTGCTGGATGAAGACTACCTTGGACAAGCAAGGCATGCTCTCCAAA
55 GTGGGAATGTGGGATTTTACATTTTCTTGTGATCGCTTGACAAATGGAAACAGCCTGGTAACACTGT
TGTGCCACCTCTTCAATACCCATGGACTCATTACCATTTCAAGTTAGATATGGTGACCTTACACCGATT
TTTAGTCATGGTTCAAGAAGATTACCACAGCCAAAACCCGTATCACAAATGCTGTTACGCAGCCGACGTC
ACCCAGGCCATGCATGCTACCTGAAAGAGCCAAAGCTTGCCAGCTTCCTCACGCCCTTGGACATCATGC
TTGGACTGCTGGCTGCAGCAGCACACGATGTGGACCACCCAGGGGTGAACCAGCCATTTTGTAAAAAAC
TAACCACCATCTTGCAAACCTATATCAGAATATGTCTGTGCTGGAGAATCATCACTGGCGATCTACAATT
60 GGCATGCTTCGAGAATCAAGGCTTCTTGTCTATTTGCCAAAGGAAATGACGTAA

stop

SEQ ID No. 5 is the amino acid sequence presented as HS_PDEXIV. For reference the sequence MM_PDEXIV is SEQ ID No. 1. CLUSTAL W (1.74) multiple sequence alignment was used.

5

10	HS_PDEXIV MM_PDEXIV	MSCLMVERCGEILFENPDQNAKVCVCM LGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYS MSCLMVERCGEVLFESPEQSVKVCVCM LGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHS *****:***.*:*.*****:***** *****:***.*
15	HS_PDEXIV MM_PDEXIV	GEIGTKKKVKRLLSFQRYFHASRLRG IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIF GEIGTKKKVKRLLSFQRYFHASRLRG IIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIF *****:*****:*****:***** *****:***** *****
20	HS_PDEXIV MM_PDEXIV	LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAAD LFDRLTNGNSLVTLCHLFNTHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAAD *****:*****:*****:***** *****:***** *****
25	HS_PDEXIV MM_PDEXIV	VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAHDVDHPGVNPFPFLIKTNHHLANLYQNMS VTQAMHCYLKEPKLASFLTPLDIMLGLLAAAHDVDHPGVNPFPFLIKTNHHLANLYQNMS *****:*****:*****:***** *****:***** *****
30	HS_PDEXIV MM_PDEXIV	VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN VLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHN *****:*****:*****:***** *****:***** *****
35	HS_PDEXIV MM_PDEXIV	KDLRLEDAQDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEIS KDLRLENDVDRHFMLQIALKCADICNPCRIWEMSKQWSERVCEEFYRQGDLEQKFELEIS *****:*****:*****:***** *****:***** *****
	HS_PDEXIV MM_PDEXIV	PLCNQQKDSIPSIQIGFMSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQ PLCNQQKDSIPSIQIGFMTYIVEPLFREWARFTGNSTLSENMLSHLAHNKAQWKSLLSNQ *****:*****:*****:***** *****:***** *****
	HS_PDEXIV MM_PDEXIV	HRSRGSSGSGPDHDHAGQGTESEEQ-EGDSP HRRRGSG-----QDLAGPAPETLEQTEGATP ** ***:*** **.*:*** **.*

1562221:5547450

SEQ ID No. 6

5 SEQ ID No. 6 is the nucleotide sequence presented as HS_PDEXIV. For reference the sequence MM_PDEXIV is SEQ ID No. 2. CLUSTAL W (1.74) multiple sequence alignment was used.

10 HS_PDEXIV -----ATGCTCTGTTTAATGGTTGAGAGGTGTGGCGAAATCTTGTTTGAGAACCCC
MM_PDEXIV -----ATGCTCTGTTTAATGGTTGAGAGGTGTGGCGAAGTCTTGTTTGAGAGCCCT

15 HS_PDEXIV GATCAGAATGCCAAATGTGTTTGCATGCTGGGAGATATACGACTAAGGGGTCAGACGGGG
MM_PDEXIV GAACAGAGTGTCAAATGTGTTTGCATGCTAGGAGATGTACGACTAAGGGGTCAGACGGGG
** **** * *****

20 HS_PDEXIV GTTCGTGCTGAACGCCGTGGCTCCTACCCATTTCATTGACTTCCGCCTACTTAACAGTACA
MM_PDEXIV GTTCCTGCCGAACGCCGTGGCTCCTACCCATTTCATTGACTTCCGTCTACTTAACAATACA

25 HS_PDEXIV ACATACTCAGGGGAGATTGGCACCAAGAAAAGGTGAAAAGACTATTAAGCTTTCAAAGA
MM_PDEXIV ACACACTCAGGGGAAATTTGGCACCAAGAAAAGGTGAAACGACTGTTAAGTTTCCAAAGA
*** *****

30 HS_PDEXIV TACTTCCATGCATCAAGGCTGCTTCGTGGAATTATACCACAAGCCCCCTCTGCACCTGCTG
MM_PDEXIV TACTTCCATGCATCTAGGCTTCTCCGGGGGATTATACCGCAGGCCCTCTCCACCTGCTG

35 HS_PDEXIV GATGAAGACTACCTTGACAAGCAAGGCATATGCTCTCCAAAGTGGGAATGTGGGATTTT
MM_PDEXIV GATGAAGACTACCTTGACAAGCAAGGCACATGCTCTCCAAAGTTGGAACGTGGGACTTT

40 HS_PDEXIV GACATTTTCTTGTTGATCGCTTGACAAATGGAAACAGCTTGGTAACACTGTTGTGCCAC
MM_PDEXIV GACATTTTCTTGTTGATCGCTTGACAAATGGGAACAGTCTGGTAACACTGTTGTGTGCAC

45 HS_PDEXIV CTCTTCAATACCCATGGACTCATTCACCATTTCAAGTTAGATATGGTGACCTTACACCGA
MM_PDEXIV CTCTTCAACTCCCATGGGCTCATCCACCATTTCAAGCTCGATATGGTGACCTTGCACAGG

50 HS_PDEXIV TTTTCTAGTCATGGTTCAAGAAGATTACCACAGCCAAACCCGTATCACAATGCTGTTCAC
MM_PDEXIV TTTCTGGTTATGGTTTCAGGAAGATTACCACGGTCACAACCCATACCACAATGCTGTTCAC
*** * * *****

55 HS_PDEXIV GCAGCCGACGTCACCCAGGCCATGCACTGCTACCTGAAAGAGCCAAAGCTTGCCAGCTTC
MM_PDEXIV GCAGCCGACGTCACCCAGGCCATGCACTGTTACCTGAAGGAGCCAAAGTTGGCAAGCTTC

60 HS_PDEXIV CTCACGCCTCTGGACATCATGCTTGGACTGCTGGCTGCAGCAGCACACGATGTGGACCAC
MM_PDEXIV CTCACACCTCTGGACATCATGCTTGGACTACTGGCTGCAGCAGCTCATGACGTGGACCAC

65 HS_PDEXIV CCAGGGGTGAACAGCCATTTTGTGATAAAACTAACCACCATCTTGCAAACCTATATCAG
MM_PDEXIV CCAGGGGTGAACAGCCATTTTGTGATAAAACTAACCACCATCTTGCAAACCTGTATCAG

70 HS_PDEXIV AATATGCTCTGTGCTGGAGAATCATCACTGGCGATCTACAATTGGCATGCTTCGAGAATCA
MM_PDEXIV AATATGCTCTGTGCTGGAGAATCACCAGTGGCGATCTACAATTGGCATGCTTCGAGAATCA

75 HS_PDEXIV AGGCTTCTTGCTCATTTGCCAAAGGAAATGACACAGGATATTGAACAGCAGCTGGGCTCC
MM_PDEXIV CGGCTCCTGGCTCACTTGCCAAAGGAAATGACACAGGATATCGAACAGCAGCTGGGCTCC

80 HS_PDEXIV TTGATCTTGGCAACAGACATCAACAGGCAGAATGAATTTTGTGACCAGATTGAAAGCTCAC
MM_PDEXIV CTCATCTTGGCCACGGATATCAACAGACAGAATGAGTTTCTGACCCGCTTAAAGCTCAC
* *****

85 HS_PDEXIV CTCCACAATAAAGACTTAAGACTGGAGGATGCACAGGACAGGCACTTTATGCTTCAGATC
MM_PDEXIV CTCCACAATAAAGATTGAGACTGGAGAATGTACAGGACAGACACTTTATGCTTCAGATC

90 HS_PDEXIV GCCTTGAAGTGTGCTGACATTTGCAATCCTTGTAAGTCTGGGAGATGAGCAAGCAGTGG
MM_PDEXIV GCCTTGAAGTGTGCTGACATTTGCAATCCTTGTCGTATCTGGGAGATGAGCAAGCAGTGG

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AGGTACGCCGTCGAGGTACCGGGTCCGGAATTCCCGGGTCGACCCACGCGTCCGGCCAGCCTCCCAGGCCGG	70
CTGCCTGCTCACCAGCCAGTGCCTAGCTCTGGGCACTGCAGCAGGCTCGGGCTCTGTCCAGCGCTCGCT	140
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TTTTCTCGAGCTCTCTGAGTCTTTGGCGTTTCTTTCTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	280
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AATCTTTCATGAACAAGCCGCACCGCTCAGAGATTTCACAGCATTCAAAGGTCACAGAACTGCCACTATGG	420
start	
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CCTCTCCACCTGCTGGATGAAGACTACCTTGGACAAGCAAGGCACATGCTCTCCAAAGTTGGAACGTGGG	770
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GCCAACTGTATCAGAATATGTCTGTAGTGGAGATCACCACCTGGCGATCTACAATTGGCATGCTTCGAG	1190
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GCACCTGTGCGGAGAACATGCTAAGCCATCTCGCGCACAACAAGCCAGTGGGAAGAGCTGCTGTCCAA	1680
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stop	
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GTCCGACTGCCCTCGCAACAAGCCCATCACGCTGGGTTTCGATGCCATCCGCTGCCACTTACCGCCTCC	1890
CTTCGTTGATCCAAGTGTACAAAAGCCATTGTACCTCAGCATTAGCTGCCGAAATGGGCGGCTCTATCC	1960
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TAGTGAGTCGTATTATAAGCTAG	2823

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start	
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CGCCGTGGCTCCTACCCATTTCATTGACTTCCGCCTACTTAAACAGTACAACATACTCAGGGGAGATTGGCA	490
CCAAGAAAAAGGTGAAAAGACTATAAGCTTTCAAAGATACCTTCCATGCATCAAGGCTGCTTCGTGGAAT	560
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TTGGACTGCTGGCTGCAGCAGCACACGATGTGGACCACCCAGGGGTGAACCAGCCATTTTGTATAAAAC	980
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stop	
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ACATACTGATGTGCATGCAGTAAAGATAAGCCACTTCTCTTAGGGCAGGCTTGGGACCTTTTGCCTGAAT	1190
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ATTGCAAGAGATTGAAGAATTAATGTGCAAAAAGAACTAAAAACTAGAGCAAAAGATCAAGTGAGAAGAA	2170
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CATCCTGTTTGTGTTACTCAATATTTCTTTCTTAAATATTCATTTACATCTATGGATTCCAATGAAAAAT	2380
ATATTTTATGTGTTCTTTGTGGAACACAGTGTATAAAATTTGTTTGGCAGAAGAAATAATTTGTATACAA	2450
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AAAAAAGAAAAAAGGGCGCCGCTCTAGAGGATCCCTCGAGGGGCCAAAGCTTACGCGTGCATGCGACG	2940
TCATAGCTCTCTCCCTATAGTGAGTCGATTTATATAAGCTAGGCATGGGCCGT	2992

SEQ ID No. 9

See Formula I

[illegible]